

Db	223	GCCGAAGCTAAAGCAAGATGCTGCTGCTGCTTGGAGACCAAGCAAGAT	282
Qy	124	ctatccacagactccagcgtatctctgaagaacatgctgaaggagcgaatgaagaa	183
Db	283	CTTATCCACACACACACAGGAGTATCTTGAAAGACATGCTGAAGAGAGCAAAATGAAGAA	342
Qy	184	gattactggagagatgaagaacagagaagaagaacaaagccattgagctccctgcaaa	243
Db	343	GATTTACTGGAGATGTAACACAGAGAGAGAAACAAAGCCATTGACTCTCTGTCAAA	402
Qy	244	gaaggaagaacccccctgaaaaaaactgtgatgtggtgagcagaagaagaatggtgaaaaat	303
Db	403	GAGAGAGAACCCCTGAAAAAACTGTGATGTGGACAGAGAGAAAGTGGTGAATTT	462
Qy	304	acatctgaataacacacagactgagagaatgcaagaagagcctgaacgattcaatgtacct	363
Db	463	ACATCTGAAATACACACAGACTGAGAGAAATGCAGAAAGGCTGAACGATTCATGTACT	522
Qy	364	gtgagcttgagagatgaagaagaagcgtcgtgagcagctaggtgttgagattcttcagttcca	423
Db	523	GTGAGCTTGGAGAGTAAAGAAAGCTGCTGGGACGTAGGTTGGGATTTCTTCAGTTCCA	582
Qy	424	acaaaagctctgcatctgatacaacaacctatggttaacttgataagcttgaaggaaga	483
Db	583	ACAAAGGCTGTGATCTGATTAACAACCTATGTTACTTGGATTAAGCTGAAGCAAGAA	642
Qy	484	gctcaagaatttggtttgaatgctcttcaatctccagaagaagcttgaagatgagagaaa	543
Db	643	GCTCAAGATTGGTTGAAATGCTCTTCAATCTCCAGAAAGCTGAAGATGATGAGAAA	702
Qy	544	ctgaaaaaagagaagagcgaattcggagattgtcaacaagtctgagcctggaacccaca	603
Db	703	CTGAAAAAGAGGAAGAGCGATTGGGATTTGTCACAACTTCACTGGAACTGGAAACCA	762
Qy	604	gaggaatacagaagcaagaagaagaagaagaagcagcgttttgagattgctcgtatgaaaa	663
Db	763	GAGATACAGAGCAAGAAAGAGAAAGAGAGAGAGCCCTTGGGATTTGCTGATGAAGAA	822
Qy	664	gtccctgatacttctctgtctccagtggtttccatcttctccctctctctgtgtacaata	723
Db	823	GTTCCTGATTAATCTTCTGTTCCAGTGTTCATTTCTTCCTCTCTGTCACATA	882
Qy	724	tatgcctaaatgacagctgcatgctcctacgtccctgacctcgaatgaggaacatgacc	783
Db	883	TATGCTTAATATGCACAGTCATGTGCTTACGTCCTCGCAATGAGGAGCATGTACCC	942
Qy	784	caagttacatccatgaactgacgtcgagcagcagcttgaactatgtctgtttcagcttgaagttg	843
Db	943	CAGGTACATCGATGAACCTGGGAGACAGCTTGAATTTGCTTTCAGCTTTAAGGTTG	1002
Qy	844	ttgtgttttgggttttgaattatgtgtgttttgaatgaagaagaagaagaagaagaaga	894
Db	1003	TTGTGTTTGTGTTTGTGATTAATGTTGCTTGAATTAATTAATTAATTAATTAATTA	1053
RESULT	3		
LOCUS	BC007099	923 bp	mRNA
DEFINITION			Homo sapiens, similar to RIKEN cDNA 1110005A23 gene, clone
ACCESSION	BC007099		MGC:14726 IMAGE:4273903, mRNA, complete cds.
VERSION	BC007099.1		GI:13937970
KEYWORDS			MGC.
SOURCE			human.
ORGANISM			Homo sapiens
REFERENCE			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS			Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE			1 (bases 1 to 923)
JOURNAL			Strausberg, R.
			Submitted (30-APR-2001) National Institutes of Health, Mammalian
			Gene Collection (MGC), Cancer Genomics Office, National Cancer

REMARK	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA			
COMMENT	NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgaps-rt@mail.nih.gov Tissue Procurement: CLONTECH cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web Site: http://www.shgc.stanford.edu Contact: (Dickson, Mark) mdickpaxil@stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.			
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.gov Series: IRAL Plate: 21 Row: 9 Column: 18 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.			
SOURCE	Location/Qualifiers 1..923 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="MGC:14726 IMAGE:4273903" /tissue_type="Prostate" /clone_lib="NIH_MGC_83" /lab_host="DH10B" /note="Vector: pDNR-LIB" 22..654 /codon_start=1 /product="Similar to RIKEN cDNA 1110005A23 gene" /protein_id="AA07099.1" /db_xref="GI:13937971" /translation="MATEYVLIHLKLAELKOECLANGLETGKIKODLIRLQAYLEHAEENAEEDVLGDETEEEKPIELPKEPEPEKTYDYAEKKVKVITSEIPIETERMOKRAERENVVLSKKKAARAARFGLSSVPTKLSNDKPMVLDLTKERAORGLNVSSISRSSEDEKIKRKERFRGIVTSSAGCTGTEDTEAKRKRRARERFGIA"			
CDS				
BASE COUNT	316 a	156 c	232 g	219 t
ORIGIN				
Query Match	99.5%	Score 889.4;	DB 9;	Length 923;
Best Local Similarity	99.9%;	Pred. No. 4e-200;		
Matches 890; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	4	agtgaagtgaagggttaacaagaatgagcagcagagcgtgagctccataaagctt	63	
Db	1	AGTGAGTGAGGGGTTAACAAAGATGGCGACCGAGCGTGGAGCTCCATTAAGCTTAAGCTT	60	
QY	64	gccgaactaaagcaagaatgtctgtctgtgtgttgtaggaaccaaggaataaagcaagat	123	
Db	61	GCCGACTAAAGCAAGATGCTTCTGCTGTGGTGGAGACCAAGGAATTAAGCAAGAT	120	
QY	124	ctatccacagactccagcgtatcttgaagaacatgcttgaagaagaggaagaagaaga	183	
Db	121	CTTATCCACAGACTCCAGCATATCTTGAAGACATGCTGAAGAGAGCAATATAAGAA	180	
QY	184	gattgacttgagagatgaagaacagagaagaagaagaacccattgaagctccctgcaaa	243	
Db	181	GATGTAAGTGGAGATGAAGAAAGAGAGAAACAAAGCCATTGACTCTCTGTCAAA	240	
QY	244	gaggaagaacccccctgaaaaaaactgtgatgtggtgagcagaagaagaatggtgaaatc	303	
Db	241	GAGGAAGAACCCCTGAAAAAACTGTGATGTGGCAGCAGAGAAAGTGGTGAATTT	300	
QY	304	acatctgaataacacacagactgagagaatgcaagaagagcctgaacgattcaatgtacct	363	
Db	301	ACATCTGAATTAACACAGCTGAGAGAAATGCAGAAAGGCTGAACGATTCATGTACT	360	
QY	364	gtgagcttgagagatgaagaagaagcgtcgtgagcagctaggtgttgagattcttcagttcca	423	

FEATURES	REMARK	COMMENT
Db	361	GTACCTTGGAGAGTAAAGAAAGCTCTCGGCGACGTAGCTTGGATTTCTTCACTTCCA 420
Oy	424	acaaaaggtctgcacatctgatacaaacactatggtttaaacttgataagctgaaggaaga 483
Db	421	ACAAAGGCTGTCTCATCTGATTAACAAACCTATGTTAGTTAACTTGAGTAACCTGAAGAAAGA 480
Oy	484	gctcaagaatttggtttgaatgctcttcacatctccagaagaagctcgaagatgatagaaga 543
Db	481	GCTCAAAATTTGGTGTAAATGTCCTTTCATCTCCAAAGTCGAAGATGATGAGAA 540
Oy	544	ctgaagaagagaagagcgaatttggaattgacaaagctcaagctcagctgagacaggaaacca 603
Db	541	CTGAAAAGAGAGAGAGAGCAGATTGGGATTTGTCACAAAGTTCAGCTGGAACTGGAAACCCACA 600
Oy	604	gaggaatacagaagcacaagaagagaaagacagaacgccttggagatgctcatalgataaa 663
Db	601	GAGGATACAGAGAGCCAAAGAAAGAGAGAGAGCGCTTGGGATTTGCCATGATGAGA 660
Oy	664	gttctgtacttcttctgtctccaaagtgtttccaatctctctctctcttctgttaacata 723
Db	661	GTCTCTGATACATTTCTGTCTTCACAGTGTCTTCATTTCTCTCTCTCTCTCTGTCACATA 720
Oy	724	tatgcctaaatgcacagatcagtgtgctcactgcctgcctccgcaatgaggagaatgtacc 783
Db	721	TATGCTTAATTCACAGTCAATGTGCTTACGCTCTGCTCTGCAATAGGAGACATGTACC 780
Oy	784	caagatcacatcagtaactgcgcgaacgaattgacttaattgctgttccagctttaaagctg 843
Db	781	CAGGATACATCCATGAACATGCGGACACAGTTTGACTTATTTGCTTTCAGCTTTAAGGTTG 840
Oy	844	ttgtgttt 894
Db	841	TTGTGTCTTTTGTCTTTTGTATTTATTTGCTTGTATTAATTAATTAATTAATTAATTAATTA 891
RESULT 4		
LOCUS	BC016941	1818 bp mRNA PRI 09-NOV-2001
DEFINITION	Homo sapiens, clone MGC:21452 IMAGE:3448446, mRNA, complete cds.	
ACCESSION	BC016941	
VERSION	BC016941.1	GI:16877383
KEYWORDS	MGC.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
AUTHORS	1 (bases 1 to 1818)	
TITLE	Strausberg, R	
JOURNAL	Direct Submission	
	Submitted (05-NOV-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	
	NIH-MGC Project URL: http://mgc.ncl.nih.gov	
	Contact: MGC help desk	
	Email: cgapbs-remail.nih.gov	
	Tissue Procurement: ATCC	
	cDNA Library Preparation: Life Technologies, Inc.	
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)	
	DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305	
	Web site: http://www.shgc.stanford.edu	
	Contact: (Dickson, Mark) mdickpaxil.stanford.edu	
	Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.	
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov	
	Series: IRAK Plate: 20 Row: a Column: 13	
	This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not Identity to protein.	
	Location/Qualifiers	

	source	1. .1818 /organism="Homo sapiens" /db_xref="taxon:9606 /clone="MGC:21452 IMAGE:344846" /tissue_type="Placenta, choriocarcinoma" /clone_id="NH_MGC_10" /lab_host="DH10B" /note="Vector: pCMV-SPORT6" 401. .1570 /codon_start=1 /product="unknown (protein for MGC:21452)" /protein_id="AAH16941.1" /db_xref="GI:16877384" /translation="MKRMAENELSRVSNEFLSKODLKKAMNTMMSRCQGHRRPE MDRPKSARFCAECNRLHPAEEDFMVESMLGKITFYALMGKVDITEMGCCORV GISDTHRVHYHSISFGSIPGTGRORATPDADPADLODLSTRFTVPQDMNGNF AASPDPAGAAASPSNSTVPKGKAEPKRKKLAELKEOCARGLETGIKODILHRLO AYLEEHAEARENEDVDGEDTEEBEERTPIELPYKEEPPKTYDAVKRKVVITSBI POTRMOKRAERENVSPVLSLKRYAKARAARGISSVPYKGLSDNNKPVRNIDKLKERQ RFGLNVSSISKSSDDDKLRKREKFIVTSAGTGTEDTEAKRRARERFGIA"
CDS		
BASE COUNT	532 a 373 c 494 g 419 t	
ORIGIN		
Query Match	93.3%; Score 833.8; DB 9; Length 1818;	
Best Local Similarity	99.8%; Pred. No. 5.7e-187;	
Matches 835:	Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
Oy	58 aagctgccgaactaaagaagtctctgtcgtggttcggagaccaggataaag	117
Dd	971 AAACCTGGCGGAACCTAAAGCAGAATGTTTGCTGCTGGTTGGAGACCAGGAATAAG	1030
Oy	118 caaga ctctatccacagactccaggcatatcttgaaagacalgtctgaagaggagcaaat	177
Dd	1031 CAAGATCTTATCCACAGACTCCAGCATATCTTGAAGAACATGCTGAAGAGAGCAAT	1090
Oy	178 gaagaagatgtacctggygagatgaaacagagaagaagaacaagccattgagctccct	237
Dd	1091 GAAGAAGATGTACTGGGAGATGAAAACAAGAGAAAGAAACCAATTGAGCTCCCT	1150
Oy	238 gtcaagaagagaagaaacccccctgaaaaaacctgttga-tgtygcagcacagaagaagaagtgtg	297
Dd	1151 GTCAANAGAGGAAGAACCCCCCTGAAAAAAGCTGTGTAATGTGGCAGCAGAAAGAAAGTGGTG	1210
Oy	298 aaaatlacatctgaaaataccacagactgagagaatgycagaagaagagggctgaaacyatlcaat	357
Dd	1211 AAAATTACATCTGGAATACACAGACTGAGAAATGACAGAAGAGGGCTGAACGATTCAT	1270
Oy	358 gtacctgtgagctctgagaaagttaagaagctcgctggcgcaagctagg ttgggatctctca	417
Dd	1271 GTACCTGTGAGCTTGGAGAGTGAAGAAAGTGTGTCGGCAGCTAGGTTTGGGATTTCTTCA	1330
Oy	418 gtccaacaaaagagctctgcatalctgataacaaacctatggtttaacttgataagctgaag	477
Dd	1331 GTTCCAACAAAAGGCTCTGTCACTGTATACAAACCTATATGGTTAACTTGGATTAAGCTGAAG	1390
Oy	478 gaaagaagctcaaagaattggtttggaatg ctctltaaatctccagagaag tgtgaagaatgat	537
Dd	1391 GAAAGAGCTCAAAGATTGGTTTGAATGTCTCTTCAATCTCCAGAAAGTCTGAAGATCAT	1450
Oy	538 gagaacactgaaaagaagaagagcgactltggagatgtcacaaagtccagctggaactgga	597
Dd	1451 GAGAAACTGAAAAMAAAGGAGAGCGGATTTGGATTGTTCACAAAGTTCAAGCTGGAACCTGGA	1510
Oy	598 acccaagaggtatacagaggaagaaagaaggaagaagagcgctttggatgtgctcga	657
Dd	1511 ACCCACAGAGGATACAGAGGCAAAAGAGGAAAGAGCAAGCAGCGCTTGGATTGCTCGA	1570
Oy	658 tgaagaagcttcgatacattctg ctctccag tg tttccattctctctctctctctgtg	717
Dd	1571 TGAAGAGTTCCGATACCTTTCGTTCTCCAGTGTTTTCATATTTCTCTCTTCTTCTTGCT	1630
Oy	718 cacatatatgctaaatgacagatcalgt g ctctac gtc ctc gtc gcaatgaaggagcat	777

Oy	778	gtaccacaggtacatcatgaactgcyggcagcaagtcttgacttatctgcgttcagcttta 837 Db
Db	1691	gtaccacaggtacatcatgaactgcyggcagcaagtcttgacttatctgcgttcagcttta 1750
Oy	838	aggattgcttcttttgtcttgatctatgcttgcttgcttaataaaaaaaatagaana 894 Db
Db	1751	AGGTTGTCTGTCTTGTCTTGTCTTGTATTCCTTGTTAATAAAAAAAATAGAAA 1807
RESULT	5	.
AC073063		
LOCUS	AC073063	84113 bp DNA linear PRI 09-JAN-2002
DEFINITION	Homo sapiens BAC clone RP11-136B3 from 7, complete sequence.	
ACCESSION	AC073063	
VERSION	AC073063.12	GI:15638765
KEYWORDS	HTG.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 84113) Title Armstrong,J., Maupin,R. and Long,N. The sequence of Homo sapiens BAC clone RP11-136B3 Unpublished (2001) 3 (bases 1 to 84113) Title Waterston,R.H. Direct Submission Submitted (08-JUN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA 4 (bases 1 to 84113) Title Waterston,R.H. Direct Submission Submitted (18-SEP-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA 5 (bases 1 to 84113) Title Waterston,R. Direct Submission Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Sep 18, 2001 this sequence version replaced g1:1331102. ----- Genome Center Center: Washington University Genome Sequencing Center Center code: WUGSC Web site: http://genome.wustl.edu/gsc Contact: saplens@wustl.wustl.edu ----- Summary Statistics Center project name: H_NH0136B03 -----	
REFERENCE		
AUTHORS		
TITLE		
JOURNAL		
COMMENT		

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

```

The sequence of this clone was established as part of a mapping and
sequencing collaboration between the NIGRI Chromosome 7 Mapping
Project (Eric D. Green, Director), John D. McPherson in the
Department of Genetics (Washington University), and the Washington
University Genome Sequencing Center. For additional information
about the map position of this sequence, see
http://www.nhgri.nih.gov/DIR/CTB/CHR7 / send
mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu/gsc

SOURCE INFORMATION:
The RPCI-11 human BAC library was made from the blood of one male
donor, as described by Osoeogawa, K., Moon, P.Y., Zhao, B., Frengen, E.,
Pateno, M., Catarese, J.J. and de Jong, P.J. (1998) An improved
approach for construction of bacterial artificial chromosome
libraries. Genomics 51:1-8. The clone may be obtained either from
Research Genetics, Inc. (http://www.resgen.com) or Pleter de Jong
and coworkers at the Roswell Park Cancer Institute
(http://bacpac.med.buffalo.edu)
VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the right is RP11-114P12, 2000 bp overlap;
the clone sequenced to the left is GSI-259H13, 200 bp overlap.
Actual start of this clone is at base position 96082 of GSI-259H13;
actual end is at base position 84113 of RP11-136B3.
location/Qualifiers
1..84113
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/db_xref="taxon:9606"
/chromosome="7"
/map="7"
/clone="RP11-136B3"
/clone_id="RPCI-11"
22..56
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46..330
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335..405
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545..613
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614..780
/rpt_family="Alu"
781..1078
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1080..1114
/rpt_family="MIR1_type"
1115..1406
/rpt_family="Alu"
1407..1540
/rpt_family="MIR1_type"
1833..2211
/note="match to EST BE147565 (NID:g8610289)"
2322..2394
/note="match to EST BE147565 (NID:g8610289)"
2337..2489
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2497..2619
/rpt_family="MIR"
2620..2644
/rpt_family="(T)n"
2926..2991
/rpt_family="MIR"
3035..3355
/rpt_family="Alu"
3374..3395
/rpt_family="(TTTCTTA)n"
3552..3852
/rpt_family="Alu"
3853..3972
/rpt_family="Alu"
4009..4388
/rpt_family="T2_type"
4419..4731

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4786..5085 /rpt_family="Alu"
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repeat_region 5239..5651 /rpt_family="L1"
repeat_region 5642..5663 /rpt_family="L1"
misc_feature 5885..6027 /note="match to EST BE795688 (NID:g10216886)"
misc_feature 5887..6025 /note="match to EST BG722929 (NID:g14002116)"
misc_feature 5887..6025 /note="match to EST BG722929 (NID:g14002116)"
misc_feature 5990..6025 /note="match to EST BG748931 (NID:g14059584)"
repeat_region 6106..6382 /rpt_family="L2"
misc_feature 6330..6334 /note="match to EST BF894562 (NID:g12286021)"
repeat_region 6683..6744 /rpt_family="Alu"
repeat_region 6745..7046 /rpt_family="L2"
repeat_region 7017..7042 /rpt_family="Alu"
repeat_region 7047..7139 /rpt_family="(GAA)n"
misc_feature 7251..7849 /rpt_family="L2"
repeat_region 7435..7732 /note="match to EST AV717144 (NID:g10814296)"
repeat_region 7735..8052 /rpt_family="Alu"
repeat_region 7907..8001 /rpt_family="Alu"
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misc_feature 8017..8086 /note="match to EST BE147565 (NID:g8610289)"
repeat_region 8118..8234 /rpt_family="A-rich"
repeat_region 8219..8241 /rpt_family="Alu"
repeat_region 8245..8543 /rpt_family="AT-rich"
misc_feature 8300..8302 /rpt_family="Alu"
repeat_region 8713..9008 /note="match to EST AV717144 (NID:g10814296)"
repeat_region 9055..9190 /rpt_family="Alu"
repeat_region 9191..9501 /rpt_family="Alu"
repeat_region 9472..9504 /rpt_family="Alu"
repeat_region 9502..9674 /rpt_family="AT-rich"
repeat_region 9648..9686 /rpt_family="Alu"
repeat_region 9714..10005 /rpt_family="(GAA)n"
repeat_region 10083..10168 /rpt_family="Alu"
repeat_region 10171..10459 /rpt_family="L1"

Query Match 72.4% Score 647.4; DB 9: length 84113;
Best Local Similarity 90.4% Pred No.6.9e-143;
Matches 782; Conservative 0; Mismatches 46; Indels 37; Gaps 7;

QY 12 gaggggtaacaagatgycgacccgagcgglytgagcttcataaagcttaagcttgcggaact 71
|||||
Db 74969 GAGGGGTAACAAGATGTAAGTACAGATGAGTGTGAGCTTCATAGCTGAAGCTGTCTAACT 75028
QY 72 aaagcaagaatgtcttgcctcgtggtttggagaccgaagggaataaagcagatcttatcca 131
|||||
Db 75029 AAAGCAAGAATGTCCTT-CTTGCTGTTTGAGACCAAGGGAATTAAGCAAGATCTTATCCA 75087
QY 132 cagactccagcagatctcttgaagaacatgctgaagaaggaggaacaaatgaagaatgact 191
|||||
Db 75088 CAGACTCCAGCATATCTTGAAGAAACATGCTTAAGAGAGGCAAAAT---GAAGATGACT 75144
QY 192 gggagatgaagaacagaggaagaacaaagcccatlgagctcccttcaaaagggaaga 251
|||||
Db 75145 AGGAGATGAACAAGAAAGAAAGAAA-----AACCCCTTGCAATATAGAGAGA 75191
QY 252 accccctg-aaaaactgttgtgtggtgcagcaggaagaagaatggttgaataataatctt 310
|||||
Db 75192 ACCCCCTGAAAAAACTGTGTGATGTGGCAGCAGAGAAAGAACTGGATGAATAATACATCTG 75251
QY 311 aataccacagactgagaagaatgcaagaaggagctgaagatccaatgactgtgagct 370
|||||
Db 75252 AAATACACAGGCTGAGAGAAATGCAGAAAGGCGCCGAACAAATTCAGTGTGAGCT 75311
QY 371 tggagagtaagaagaagctgctcgagcagctaggcttggatcttcacgttccacaagaag 430
|||||
Db 75312 TCGAGGTAAAGAAAGCTGCTCAGCAGCAGTACGTTTGAGTTCAGTTCACAAAGAAA- 75370
QY 431 gctgtcatctgtatacaaacctatggttaacttgatgaagcttgaagaagaagctcaaa 490
|||||
Db 75371 GCTGTGATCTG- -AACACACTATGTTAACTTGATTAAGCCGAAGAAAGAGCTCAAA 75428
QY 491 gatttggttgatgtctcttcacatccagaagaatctgaagaatgatgaaactgaa 550
|||||
Db 75429 GATTGTTGTTGAATGCTCTTCAATTTCCAGAAAGTCAAGATATATAAGAAACCTGAAA 75488
QY 551 aagaagaagaagcagatctggagatgtcaaaagctcagctggaactggaaccacagagata 610
|||||
Db 75489 ACAGGAAGAGCGATTTGGAGTTGTACAAAGTTCAGTGAAGCTGAACACAGAGAGATA 75548
QY 611 cagaagcagaagaagaagaagaagcagcgtttggagatgcccgaatgaaagatcctg 670
|||||
Db 75549 CAGAGCAAAAGAGAGAAAGAGAGAGAGAGCGCTTTGGCTTCGATGAAGAAAGTCTTG 75608
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LOCUS Homo sapiens chromosome 8 clone RP11-262017 map 8, WORKING DRAFT
DEFINITION SEQUENCE, 4 unordered pieces.
ACCESSION AC022200
VERSION AC022200.6 GI:13518207
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

AP001207 153936 bp DNA linear PRI 24-JUN-2000
 LOCUS Homo sapiens genomic DNA, chromosome 8q23, clone:KB1562D12.
 ACCESSION AP001207
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 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 153936)
 AUTHORS Shimizu,N and Asakawa,S.
 JOURNAL Homo sapiens chromosome clone BAC KB1562D12 on 8q23
 REFERENCE 2 (bases 1 to 153936)
 AUTHORS Shimizu,N. and Asakawa,S.
 TITLE Direct Submission
 JOURNAL Submitted (21-FEB-2000) to the DDBJ/EMBL/GenBank databases.
 Nobuyoshi Shimizu, Keio University, School of Medicine, Molecular
 Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo 160-8582, Japan
 (E-mail:nshimizu@med.keio.ac.jp, Tel:81-3-3351-2370,
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 COMMENT On Jun 24, 2000 this sequence version replaced gi:8096488.
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LOCUS	AC091052/C	RESULT 8
DEFINITION	AC091052	166471 bp DNA linear
ACCESSION	AC091052	HTG 25-MAR-2001
KEYWORDS	AC091052.1 GI:13446282	
SOURCE	HTG: HTGS_PHASE1: HTGS_DRAFT.	
ORGANISM	human.	
REFERENCE	Mumukshya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	1 (bases 1 to 166471)	
TITLE	Birren,B., Linton,L., Nusbaum,C. and Lander,E.	
JOURNAL	Homo sapiens chromosome 8, clone RP11-373122	
AUTHORS	Unpublished	
	2 (bases 1 to 166471)	
	Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S., Barra,N., Bastien,V., Boguslavskiy,L., Bouckgalter,B., Brown,A., Cammarata,J., Campopiano,A., Chang,J., Choepiel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., Deavellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Glinde,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Karatas,A., LaRoque,K., Lamaizares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G., McClean,C., Macdonald,P., Marquis,N., Matthews,C., McCarthy,M., McKean,P., McKernan,K., McPheters,R., Melgrim,J., Meneus,L., Milnova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Notman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Roestli,M., Roy,A., Santos,R., Schauer,S., Schupbach,R., Seaman,S.,	

REFERENCE Mammalia: Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 149312)
 AUTHORS Waterston, R.H.
 TITLE The sequence of Homo sapiens clone
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 149312)
 . AUTHORS Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (14-JUN-2000) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA

COMMENT

----- Genome Center -----
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu/gsc/index.shtml
 ----- Project Information -----
 Center project name: H_NH0373L22
 ----- Summary Statistics -----
 Sequencing vector: M13; 100%
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Chemistry: Dye-terminator Big Dye; 0% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 131361 bases at least Q40
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 Insert size: 145000; agarose-fp
 Insert size: 145612; sum-of-contigs
 Quality coverage: 3.09 in Q20 bases; agarose-fp
 Quality coverage: 3.17 in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 38 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
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 * 3559 5237: contig of 1579 bp in length
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KEYWORDS		HTG.	
SOURCE		human.	
ORGANISM		Homo sapiens	
REFERENCE		Enxarxola, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
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		Vinson,R., Wall,R., Wang,S., Ward-Moore,S., Warren,R.,	
		Washington,C., Watlington,S., Williams,G., Williamson,A	
		Wlaczek,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J.,	
		Zorilla,S., Zuckierapatti,R., Weinstein,G. and Gibbs,R.	
TITLE		Direct Submission	
JOURNAL		Unpublished	
REFERENCE		2 (bases 1 to 54666)	
AUTHORS		Worley,K.C.	

TITLE	Direct Submission
JOURNAL	Submitted (19-JUN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE AUTHORS	3 (bases 1 to 54666) Morley,K.C.
TITLE	Direct Submission
JOURNAL	Submitted (30-JUN-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE AUTHORS	4 (bases 1 to 54666) Morley,K.C.
TITLE	Direct Submission
JOURNAL	Submitted (03-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT	On Jun 30, 2001 this sequence version replaced gi:14575758. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids. Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as low Coverage.

QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

QUALSTAT-REPORT.

FEATURES	Location/Qualifiers
source	1..54666 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="12" /clone="Rp11-76217" 8..292 repeat_region /rpt_family="Alusp" 293..3320 repeat_region /rpt_family="(CAA)n" 337..454 repeat_region /rpt_family="Alub" 456..734 repeat_region complement(1548..1602) /rpt_family="LZ" repeat_region complement(4116..4163) /rpt_family="MIR"

repeat_region	1164. .4445	/rpt_family="AluXs"
repeat_region	complement(4446. .4588)	/rpt_family="MIR"
repeat_region	complement(4643. .5004)	/rpt_family="L2"
repeat_region	5027. .5086	/rpt_family="(TTTTC)n"
repeat_region	complement(5096. .5404)	/rpt_family="AluXs"
repeat_region	complement(5738. .5799)	/rpt_family="MIR"
repeat_region	complement(6208. .6518)	/rpt_family="AluY"
repeat_region	7220. .7355	/rpt_family="C-rich"
repeat_region	7583. .7801	/rpt_family="CT-rich"
repeat_region	7925. .7977	/rpt_family="(CCCC)n"
repeat_region	8037. .8076	/rpt_family="C-rich"
repeat_region	8212. .8251	/rpt_family="(CGG)n"
repeat_region	10383. .10412	/rpt_family="(GGGGA)n"
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STS	14988. .15146	/standard_name="37028"
repeat_region	15260. .15281	/rpt_family="AT-rich"
repeat_region	16229. .16286	/rpt_family="MIR"
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STS	16559. .16661	/standard_name="36508"
STS	16927. .17081	/standard_name="87392"
repeat_region	18299. .18606	/rpt_family="AluSc"
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repeat_region	complement(19482. .19685)	/rpt_family="MIR"
STS	21682. .21805	/standard_name="73682"
STS	22161. .22330	/standard_name="4986"
STS	22219. .22335	/standard_name="14903"
repeat_region	23176. .23469	/rpt_family="AluSg"
repeat_region	23543. .23715	/rpt_family="MSTA"
repeat_region	complement(23717. .23966)	/rpt_family="AluXs"
repeat_region	complement(24106. .24219)	/rpt_family="MIR"
repeat_region	complement(24220. .24394)	/rpt_family="AluXs"
repeat_region	24395. .24423	/rpt_family="(TAAA)n"
repeat_region	complement(24424. .24551)	

QY	612	agaagcaagaagagaaagaagacagagcgtcttggagctgcctgatgataaagtcctga	671
Db	22368	ACAGGCAAGAAAGAGAAAGAAAGCAGACCGCTTGGCGATTCCTCGATGATAAAGTCCCTGA	22309
QY	672	tacttcgtctctccagtgctttccattctctctctctctctctctcttcttggtcaatatagccta	731
Db	22308	TACTTTCGTTCTCCAGTGTTTCCATTCTCTCTTCTTGTGGTCACATATATAGCTTA	22249
QY	732	aatgcacagcatatgctcctacgcctcgtcctgcagatgagggagacatgataccaccagtlaca	791
Db	22248	AATGCACAGTCATGCGCTACGTCCTCGCTCGCAATGAGGAGCATGACCCAGGTACCA	22189
QY	792	tccatgaactcgcgcgaagaagtttgacttatgctgcgtttcaagctttaagttgtgtgtct	851
Db	22188	TCCATGAACCTCGGAGAGATTTGACTTATGCTGTTTACACTTAAAGCTGTGTGTCTT	22129
QY	852	ttgttttgattcatgcttgcctgttcaataaaaaaaataaga	894
Db	22128	TTGTTTTGATTATGTTCTCTGTTATATAAAAAAATGAAAA	22086
RESULT	12		
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LOCUS	Homo sapiens chromosome 12 clone RP11-670P16,	WORKING DRAFT	
DEFINITION	SEQUENCE, 20 unordered pieces.		
ACCESSION	AC023055		
VERSION	AC023055.20	GI:12083915	
KEYWORDS	HTG; HTGS-PHASE1; HTGS-DRAFT; HTGS-FULLTOP.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo. 1 (bases 1 to 200379)		
AUTHORS	Muzny,D.M., Adams,C., Adio-Oduola,B., All-oman,F.R., Allen,C., Alsbrooks,S.L., Amaralung,H.C., Are,J.R., Banks,T., Barbarta,J., Benton,J., Blmage,K., Blankenburg,K., Bonlin,D., Bouck,J., Bowie,S., Brieava,M., Brown,E., Brown,M., Bryant,N.P., Buhey,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavaros,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy,Carol,L., Dederich,D.A., Delaney,K.R., Delgado,O., Dem,A.L., Ding,Y., Dinu,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogue,M., Holloway,C., Hollins,B., Homs,I.F., Howard,S., Huber,J., Hultj,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudan,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Licharge,O., Lieu,C., Liu,J., Liu,W., Lonslegd,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhinney,E., Mcleod,M.P., Meador,M., Mel,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Norkenwo,S., Oguh,M., Okwoung,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Peters,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Oulles,M., Ren,Y., Rivers,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherrer,S., Scott,G., Shen,H., Shooshari,N., Sisson,I., Sodegren,E., Sonlike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Teliro,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalton,D., Vinson,R., Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.		

TITLE
JOURNAL
COMMENT

Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Rella, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Triggillo, J., Vassiliev, H.,
Vial, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (10-JAN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L18853
Center clone name: 320_D_22

* NOTE: This record contains 74 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

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* 3282 4002: contig of 721 bp in length
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* 4804 4903: gap of 100 bp
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* 5715 6430: contig of 716 bp in length
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RESULT 15
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LOCUS Sequence 531 from Patent WO0157058.
DEFINITION AX210889
ACCESSION AX210889
VERSION AX210889.1 GI:15425149
KEYWORDS
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ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 255)
AUTHORS Rosenthal, A., Hinzmann, B., Schaefer, R., Zuber, J., Tchernitsa, O.,
Grips, M., Hellriegel, M., Schmitz, A.C. and Sers, C.
TITLE Detection of differential gene expression
JOURNAL Patent: WO 0157058-A 531 09-AUG-2001.
Metagen Gesellschaft fuer Genomforschung mbH (DE)
FEATURES
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Location/Qualifiers
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ORIGIN

Query Match 23.7%; Score 211.8; DB 6; Length 255;
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Matches 228; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

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Db 181 CTTGGAGAGTAAGAGCTGCTCGGGCAGCGAGGTTTGAATTCTCAGTTCACAACAAA 240
OY 429 agtctgtcatctga 443
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Db 241 AGTTTATCATCTCTGA 255

Search completed: June 19, 2002, 14:23:34
Job time: 9027 sec